

SEQUENCE LISTING

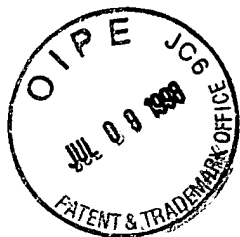
(1) GENERAL INFORMATION

- (i) APPLICANT: Ruvkun, Gary
Morris, Jason
Tissenbaum, Heidi
- (ii) TITLE OF THE INVENTION: AGE-1 POLYPEPTIDES AND RELATED
MOLECULES AND METHODS
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Clark & Elbing LLP
(B) STREET: 176 Federal Street
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02110
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US97/13914
(B) FILING DATE: 07-AUG-1997
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/023,382
(B) FILING DATE: 07-AUG-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Elbing, Karen L
(B) REGISTRATION NUMBER: 35,238
(C) REFERENCE/DOCKET NUMBER: 08472/704WO2
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 617-428-0200
(B) TELEFAX: 617-428-7045
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1146 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met His Val Asn Ile Leu His Pro Gln Leu Gln Thr Met Val Glu Gln
1 5 10 15



Trp	Gln	Met	Arg	Glu	Arg	Pro	Ser	Leu	Glu	Thr	Glu	Asn	Gly	Lys	Gly
			20					25					30		
Ser	Leu	Leu	Leu	Glu	Asn	Glu	Gly	Val	Ala	Asp	Ile	Ile	Thr	Met	Cys
		35					40					45			
Pro	Phe	Gly	Glu	Val	Ile	Ser	Val	Val	Phe	Pro	Trp	Phe	Leu	Ala	Asn
	50					55					60				
Val	Arg	Thr	Ser	Leu	Glu	Ile	Lys	Leu	Ser	Asp	Phe	Lys	His	Gln	Leu
65					70					75				80	
Phe	Glu	Leu	Ile	Ala	Pro	Met	Lys	Trp	Gly	Thr	Tyr	Ser	Val	Lys	Pro
				85					90					95	
Gln	Asp	Tyr	Val	Phe	Arg	Gln	Leu	Asn	Asn	Phe	Gly	Glu	Ile	Glu	Val
			100					105					110		
Ile	Phe	Asn	Asp	Asp	Gln	Pro	Leu	Ser	Lys	Leu	Glu	Leu	His	Gly	Thr
		115					120					125			
Phe	Pro	Met	Leu	Phe	Leu	Tyr	Gln	Pro	Asp	Gly	Ile	Asn	Arg	Asp	Lys
	130						135				140				
Glu	Leu	Met	Ser	Asp	Ile	Ser	His	Cys	Leu	Gly	Tyr	Ser	Leu	Asp	Lys
145					150					155				160	
Leu	Glu	Glu	Ser	Leu	Asp	Glu	Glu	Leu	Arg	Gln	Phe	Arg	Ala	Ser	Leu
				165					170					175	
Trp	Ala	Arg	Thr	Lys	Lys	Thr	Cys	Leu	Thr	Arg	Gly	Leu	Glu	Gly	Thr
			180					185					190		
Ser	His	Tyr	Ala	Phe	Pro	Glu	Glu	Gln	Tyr	Leu	Cys	Val	Gly	Glu	Ser
		195					200					205			
Cys	Pro	Lys	Asp	Leu	Glu	Ser	Lys	Val	Lys	Ala	Ala	Lys	Leu	Ser	Tyr
	210					215					220				
Gln	Met	Phe	Trp	Arg	Lys	Arg	Lys	Ala	Glu	Ile	Asn	Gly	Val	Cys	Glu
225					230					235				240	
Lys	Met	Met	Lys	Ile	Gln	Ile	Glu	Phe	Asn	Pro	Asn	Glu	Thr	Pro	Lys
				245					250					255	
Ser	Leu	Leu	His	Thr	Phe	Leu	Tyr	Glu	Met	Arg	Lys	Leu	Asp	Val	Tyr
			260					265					270		
Asp	Thr	Asp	Asp	Pro	Ala	Asp	Glu	Gly	Trp	Phe	Leu	Gln	Leu	Ala	Gly
		275					280					285			
Arg	Thr	Thr	Phe	Val	Thr	Asn	Pro	Asp	Val	Lys	Leu	Thr	Ser	Tyr	Asp
					295						300				
Gly	Val	Arg	Ser	Glu	Leu	Glu	Ser	Tyr	Arg	Cys	Pro	Gly	Phe	Val	Val
305					310					315				320	
Arg	Arg	Gln	Ser	Leu	Val	Leu	Lys	Asp	Tyr	Cys	Arg	Pro	Lys	Pro	Leu
				325					330					335	
Tyr	Glu	Pro	His	Tyr	Val	Arg	Ala	His	Glu	Arg	Lys	Leu	Ala	Leu	Asp
			340					345					350		
Val	Leu	Ser	Val	Ser	Ile	Asp	Ser	Thr	Pro	Lys	Gln	Ser	Lys	Asn	Ser
		355					360					365			
Asp	Met	Val	Met	Thr	Asp	Phe	Arg	Pro	Thr	Ala	Ser	Leu	Lys	Gln	Val
	370					375					380				
Ser	Leu	Trp	Asp	Leu	Asp	Ala	Asn	Leu	Met	Ile	Arg	Pro	Val	Asn	Ile
385					390					395				400	
Ser	Gly	Phe	Asp	Phe	Pro	Ala	Asp	Val	Asp	Met	Tyr	Val	Arg	Ile	Glu
				405					410					415	
Phe	Ser	Val	Tyr	Val	Gly	Thr	Leu	Thr	Leu	Ala	Ser	Lys	Ser	Thr	Thr
			420					425					430		
Lys	Val	Asn	Ala	Gln	Phe	Ala	Lys	Trp	Asn	Lys	Glu	Met	Tyr	Thr	Phe
		435					440					445			
Asp	Leu	Tyr	Met	Lys	Asp	Met	Pro	Pro	Ser	Ala	Val	Leu	Ser	Ile	Arg
	450					455					460				
Val	Leu	Tyr	Gly	Lys	Val	Lys	Leu	Lys	Ser	Glu	Glu	Phe	Glu	Val	Gly
465					470					475				480	
Trp	Val	Asn	Met	Ser	Leu	Thr	Asp	Trp	Arg	Asp	Glu	Leu	Arg	Gln	Gly
				485					490					495	
Gln	Phe	Leu	Phe	His	Leu	Trp	Ala	Pro	Glu	Pro	Thr	Ala	Asn	Arg	Ser
			500					505					510		
Arg	Ile	Gly	Glu	Asn	Gly	Ala	Arg	Ile	Gly	Thr	Asn	Ala	Ala	Val	Thr
		515					520					525			
Ile	Glu	Ile	Ser	Ser	Tyr	Gly	Gly	Arg	Val	Arg	Met	Pro	Ser	Gln	Gly

530	Gln Tyr Thr Tyr Leu Val	535	Lys His Arg Ser Thr	540	Trp Thr Glu Thr Leu
545	Asn Ile Met Gly Asp	550	Tyr Glu Ser Cys Ile	555	Arg Asp Pro Gly Tyr
	565		570		575
Lys Lys Leu Gln Met Leu Val Lys Lys His Glu Ser Gly Ile Val Leu	580	585	590		
Glu Glu Asp Glu Gln Arg His Val Trp Met Trp Arg Arg Tyr Ile Gln	595	600	605		
Lys Gln Glu Pro Asp Leu Leu Ile Val Leu Ser Glu Leu Ala Phe Val	610	615	620		
Trp Thr Asp Arg Glu Asn Phe Ser Glu Leu Tyr Val Met Leu Glu Lys	625	630	635		640
Trp Lys Pro Pro Ser Val Ala Ala Ala Leu Thr Leu Leu Gly Lys Arg	645	650	655		
Cys Thr Asp Arg Val Ile Arg Lys Phe Ala Val Glu Lys Leu Asn Glu	660	665	670		
Gln Leu Ser Pro Val Thr Phe His Leu Phe Ile Leu Pro Leu Ile Gln	675	680	685		
Ala Leu Lys Tyr Glu Pro Arg Ala Gln Ser Glu Val Gly Met Met Leu	690	695	700		
Leu Thr Arg Ala Leu Cys Asp Tyr Arg Ile Gly His Arg Leu Phe Trp	705	710	715		720
Leu Leu Arg Ala Glu Ile Ala Arg Leu Arg Asp Cys Asp Leu Lys Ser	725	730	735		
Glu Glu Tyr Arg Arg Ile Ser Leu Leu Met Glu Ala Tyr Leu Arg Gly	740	745	750		
Asn Glu Glu His Ile Lys Ile Ile Thr Arg Gln Val Asp Met Val Asp	755	760	765		
Glu Leu Thr Arg Ile Ser Thr Leu Val Lys Gly Met Pro Lys Asp Val	770	775	780		
Ala Thr Met Lys Leu Arg Asp Glu Leu Arg Ser Ile Ser His Lys Met	785	790	795		800
Glu Asn Met Asp Ser Pro Leu Asp Pro Val Tyr Lys Leu Gly Glu Met	805	810	815		
Ile Ile Asp Lys Ala Ile Val Leu Gly Ser Ala Lys Arg Pro Leu Met	820	825	830		
Leu His Trp Lys Asn Lys Asn Pro Lys Ser Asp Leu His Leu Pro Phe	835	840	845		
Cys Ala Met Ile Phe Lys Asn Gly Asp Asp Leu Arg Gln Asp Met Leu	850	855	860		
Val Leu Gln Val Leu Glu Val Met Asp Asn Ile Trp Lys Ala Ala Asn	865	870	875		880
Ile Asp Cys Cys Leu Asn Pro Tyr Ala Val Leu Pro Met Gly Glu Met	885	890	895		
Ile Gly Ile Ile Glu Val Val Pro Asn Cys Lys Thr Ile Phe Glu Ile	900	905	910		
Gln Val Gly Thr Gly Phe Met Asn Thr Ala Val Arg Ser Ile Asp Pro	915	920	925		
Ser Phe Met Asn Lys Trp Ile Arg Lys Gln Cys Gly Ile Glu Asp Glu	930	935	940		
Lys Lys Lys Ser Lys Lys Asp Ser Thr Lys Asn Pro Ile Glu Lys Lys	945	950	955		960
Ile Asp Asn Thr Gln Ala Met Lys Lys Tyr Phe Glu Ser Val Asp Arg	965	970	975		
Phe Leu Tyr Ser Cys Val Gly Tyr Ser Val Ala Thr Tyr Ile Met Gly	980	985	990		
Ile Lys Asp Arg His Ser Asp Asn Leu Met Leu Thr Glu Asp Gly Lys	995	1000	1005		
Tyr Val His Ile Asp Phe Gly His Ile Leu Gly His Gly Lys Thr Lys	1010	1015	1020		
Leu Gly Ile Gln Arg Asp Gln Pro Phe Ile Leu Thr Glu His Phe	1025	1030	1035		1040
Met Thr Val Ile Arg Ser Gly Lys Ser Val Asp Gly Asn Ser His Glu	1045	1050	1055		

Leu Gln Lys Phe Lys Thr Leu Cys Val Glu Ala Tyr Glu Val Met Trp
 1060 1065 1070
 Asn Asn Arg Asp Leu Phe Val Ser Leu Phe Thr Leu Met Leu Gly Met
 1075 1080 1085
 Glu Leu Pro Glu Leu Ser Thr Lys Ala Asp Leu Asp His Leu Lys Lys
 1090 1095 1100
 Thr Leu Phe Cys Asn Gly Glu Ser Lys Glu Glu Ala Arg Lys Phe Phe
 105 1110 1115 1120
 Ala Gly Ile Tyr Glu Glu Ala Phe Asn Gly Ser Trp Ser Thr Lys Thr
 1125 1130 1135
 Asn Trp Leu Phe His Ala Val Lys His Tyr
 1140 1145

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGGAAGCCAT	GGAGCTCGAG	ATCTGATTGC	TGGACACGGA	CGGAACTCCG	ACGTATCTCG	60
CAGATGCATG	TTAACATTTT	ACATCCACAA	CTGCAAACGA	TGGTCGAGCA	GTGGCAAATG	120
CGAGAACGCC	CATCGCTGGA	GACCGAGAAT	GGCAAAGGAT	CGCTGCTCCT	GGAAAATGAA	180
GGTGTGCGAG	ATATCATCAC	TATGTGTCCA	TTCGGAGAAG	TTATTAGTGT	AGTATTTCCG	240
TGGTTTCTTG	CAAATGTGCG	AACATCGCTA	GAAATCAAGC	TATCAGATTT	CAAACATCAA	300
CTTTTCGAAT	TGATTGCTCC	GATGAAGTGG	GGAACATATT	CCGTAAAGCC	ACAGGATTAT	360
GTGTTTCAGAC	AGTTGAATAA	TTTCGGCGAA	ATTGAAGTTA	TATTTAAACGA	CGATCAACCC	420
CTGTGCGAAAT	TAGAGCTCCA	CGGCACCTTC	CCAATGCTTT	TTCTCTACCA	ACCTGATGGA	480
ATAAACAGGG	ATAAAGAATT	AATGAGTGAT	ATAAGTCATT	GTCTAGGATA	CTCACTGGAT	540
AAACTGGAAG	AGAGCCTCGA	TGAGGAACTC	CGTCAATTTT	GTGCTTCTCT	CTGGGCTCGT	600
ACGAAGAAAA	CGTGCTTGAC	ACGTGGACTT	GAGGGTACCA	GTCACTACGC	GTTCCCCGAA	660
GAACAGTACT	TGTGTGTTGG	TGAATCGTGC	CCGAAAGATT	TGGAATCAAA	AGTCAAGGCT	720
GCCAAGCTGA	GTTATCAGAT	GTTTTGGAGA	AAACGTAAG	CGGAAATCAA	TGGAGTTTGC	780
GAGAAAATGA	TGAAGATTCA	AATTGAATTC	AATCCGAACG	AAACTCCGAA	ATCTCTGCTT	840
CACACGTTTC	TCTACGAAAT	GCGAAAATTG	GATGTATACG	ATACCGATGA	TCCTGCAGAT	900
GAAGGATGGT	TTCTTCAATT	GGCTGGACGT	ACCACGTTTG	TTACAAATCC	AGATGTCAAA	960
CTTACGTCTT	ATGATGGTGT	CCGTTCGGAA	CTGGAAAGCT	ATCGATGCCC	TGGATTTCGTT	1020
GTTCGCCGAC	AATCACTAGT	CCTCAAAGAC	TATTGTTCGCC	CAAACCACT	CTACGAACCA	1080
CATTATGTGA	GAGCACACGA	ACGAAAACCT	GCTCTAGACG	TGCTCAGCGT	GTCTATAGAT	1140
AGCACACCAA	AACAGAGCAA	GAACAGTGAT	ATGGTTATGA	CTGATTTTCG	TCCGACAGCT	1200
TCACTCAAAC	AAGTTTCACT	TTGGGACCTT	GACGCGAATC	TTATGATACG	GCCTGTGAAT	1260
ATTTCTGGAT	TCGATTTCCC	GGCCGACGTG	GATATGTACG	TTCGAATCGA	ATTCAAGTGA	1320
TATGTGGGGA	CACTGACGCT	GGCATCAAAA	TCTACAACAA	AAGTGAATGC	TCAATTTGCA	1380
AAATGGAATA	AGGAAATGTA	CACTTTTGAT	CTATACATGA	AGGATATGCC	ACCATCTGCA	1440
GTACTCAGCA	TTCTGTGTTT	GTACGGAAAA	GTGAAATTAA	AAAGTGAAGA	ATTCGAAGTT	1500
GGTTGGGTAA	ATATGTCCCT	AACCGATTGG	AGAGATGAAC	TACGACAAGG	ACAATTTTTA	1560
TTCCATCTGT	GGGCTCCTGA	ACCGACTGCC	AATCGTAGTA	GGATCGGAGA	AAATGGAGCA	1620
AGGATAGGCA	CCAACGCAGC	GGTTACAATT	GAAATCTCAA	GTTATGGTGG	TAGAGTTCTGA	1680
ATGCCGAGTC	AAGGACAATA	CACATATCTC	GTCAAGCACC	GAAGTACTTG	GACGGAAACT	1740
TTGAATATTA	TGGGTGATGA	CTATGAGTCG	TGTATCAGAG	ATCCAGGATA	TAAGAAGCTT	1800
CAGATGCTTG	TCAAGAAGCA	TGAATCTGGA	ATTGTATTAG	AGGAAGATGA	ACAACGTCAT	1860
GTCTGGATGT	GGAGGAGATA	CATTCAAAAG	CAGGAGCCTG	ATTTGCTCAT	TGTGCTCTCC	1920
GAACTCGCAT	TTGTGTGGAC	TGATCGTGAG	AACTTTTCCG	AGCTCTATGT	GATGCTTGAA	1980
AAATGGAAAC	CGCCGAGTGT	GGCAGCCGCG	TTGACTTTGC	TTGGAAAACG	TTGCACGGAT	2040
CGTGTGATTG	GAAAGTTTGC	AGTGGAGAAG	TTGAATGAGC	AGCTGAGCCC	GGTCACATTC	2100
CATCTTTTCA	TATTGCCTCT	CATACAGGCG	TTGAAGTACG	AACCGCGTGC	TCAATCGGAA	2160
GTTGGAATGA	TGCTCTTGAC	TAGAGCTCTC	TGCGATTATC	GAATTGGACA	TGCACTTTTC	2220
TGGTGCTCTC	GTGCAGAGAT	TGCTCGTTTG	AGAGATTGTG	ATCTGAAAAG	TGAAGAATAT	2280
CGCCGTATCT	CACTTCTGAT	GGAAGCTTAC	CTCCGTGGAA	ATGAAGAGCA	CATCAAGATC	2340
ATCACCCGAC	AAGTTGACAT	GGTTGATGAG	CTCACACGAA	TCAGCACTCT	TGTCAAAGGA	2400

ATGCCAAAAG	ATGTTGCTAC	GATGAAACTG	CGTGACGAGC	TTCGATCGAT	TAGTCATAAA	2460
ATGGAAAATA	TGGATTCTCC	ACTGGATCCT	GTGTACAAAC	TGGGTGAAAT	GATAATCGAC	2520
AAAGCCATCG	TCCTAGGAAG	TGCAAAACGT	CCGTTAATGC	TTCACTGGAA	GAACAAAAAT	2580
CCAAAGAGTG	ACCTGCACCT	TCCGTTCTGT	GCAATGATCT	TCAAGAATGG	AGACGATCTT	2640
CGCCAGGACA	TGCTTGTTCT	TCAAGTTCTC	GAAGTTATGG	ATAACATCTG	GAAGGCTGCA	2700
AACATTGATT	GCTGTTTGAA	CCCGTACGCA	GTTCTTCCAA	TGGGAGAAAT	GATTGGAATT	2760
ATTGAAGTTG	TGCCTAATTG	TAAAACAATA	TTCGAGATTC	AAGTTGGAAC	AGGATTCATG	2820
AATACAGCAG	TTCGGAGTAT	TGATCCTTCG	TTTATGAATA	AGTGGATTCTG	GAAACAATGC	2880
GGAATTGAAG	ATGAAAAGAA	GAAAAGCAAA	AAGGACTCTA	CGAAAAATCC	CATCGAAAAG	2940
AAGATTGATA	ATACTCAAGC	CATGAAGAAA	TATTTTGAAA	GTGTCGATCG	ATTCCTATAC	3000
TCGTGTGTTG	GATATTCAGT	TGCCACGTAC	ATAATGGGAA	TCAAGGATCG	TCACAGTGAT	3060
AATCTGATGC	TCACTGAAGA	TGGAAAATAT	GTCCACATTG	ATTTTCGGTCA	CATTTTGGGA	3120
CACGGAAAGA	CCAAACTTGG	GATCCAGCGA	GATCGTCAAC	CGTTTATTCT	AACCGAACAC	3180
TTTATGACAG	TGATTTCGATC	GGGTAAATCT	GTGGATGGAA	ATTCGCATGA	GCTACAAAAA	3240
TTCAAAACGT	TATGCGTCGA	AGCCTACGAA	GTAATGTGGA	ATAATCGAGA	TTTGTTTCGTT	3300
TCCTTGTTCA	CCTTGATGCT	CGGAATGGAG	TTGCCTGAGC	TGTCGACGAA	AGCGGATTTG	3360
GATCATTTGA	AGAAAACCCT	CTTCTGCAAT	GGAGAAAGCA	AAGAAGAAGC	GAGAAAGTTT	3420
TTCGCTGGAA	TCTACGAAGA	AGCCTTCAAT	GGATCATGGT	CTACCAAAAC	GAATTGGCTC	3480
TTCCACGCAG	TCAAACACTA	CTGA				3504

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCTGGTTCA TTTCCCAACC 20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGTAACCTCAC CTAGTCTTCG 20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AACAATTACA GGCCGATCC 19

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: Other
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
 ATGCCACGCA AGAAACTCAC 20

(2) INFORMATION FOR SEQ ID NO:7:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: Other
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
 GAAAAGATGG AATGTGACCG 20

(2) INFORMATION FOR SEQ ID NO:8:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: Other
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
 ATCTGAAGCG TTCTTATATC 20

(2) INFORMATION FOR SEQ ID NO:9:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: Other
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
 TGCTCCATTT TCTCCGATCC 20

(2) INFORMATION FOR SEQ ID NO:10:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1068 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Pro	Pro	Arg	Pro	Ser	Ser	Gly	Glu	Leu	Trp	Gly	Ile	His	Leu	Met
1				5					10					15	
Pro	Pro	Arg	Ile	Leu	Val	Glu	Cys	Leu	Leu	Pro	Asn	Gly	Met	Ile	Val
			20					25					30		
Thr	Leu	Glu	Cys	Leu	Arg	Glu	Ala	Thr	Leu	Val	Thr	Ile	Lys	His	Glu
		35					40					45			
Leu	Phe	Arg	Glu	Ala	Arg	Lys	Tyr	Pro	Leu	His	Gln	Leu	Leu	Gln	Asp
	50					55					60				
Glu	Thr	Ser	Tyr	Ile	Phe	Val	Ser	Val	Thr	Gln	Glu	Ala	Glu	Arg	Glu
65					70					75					80
Glu	Phe	Phe	Asp	Glu	Thr	Arg	Arg	Leu	Cys	Asp	Leu	Arg	Leu	Phe	Gln
			85						90					95	
Pro	Phe	Leu	Lys	Val	Ile	Glu	Pro	Val	Gly	Asn	Arg	Glu	Glu	Lys	Ile
			100					105					110		
Leu	Asn	Arg	Glu	Ile	Gly	Phe	Val	Ile	Gly	Met	Pro	Val	Cys	Glu	Phe
		115					120					125			
Asp	Met	Val	Lys	Asp	Pro	Glu	Val	Gln	Asp	Phe	Arg	Arg	Asn	Ile	Leu
	130					135					140				
Asn	Val	Cys	Lys	Glu	Ala	Val	Asp	Leu	Arg	Asp	Leu	Asn	Ser	Pro	His
145					150					155					160
Ser	Arg	Ala	Met	Tyr	Val	Tyr	Pro	Pro	Asn	Val	Glu	Ser	Ser	Pro	Glu
			165						170					175	
Leu	Pro	Lys	His	Ile	Tyr	Asn	Lys	Leu	Asp	Lys	Gly	Gln	Ile	Ile	Val
			180					185					190		
Val	Ile	Trp	Val	Ile	Val	Ser	Pro	Asn	Asn	Asp	Lys	Gln	Lys	Tyr	Thr
	195						200					205			
Leu	Lys	Ile	Asn	His	Asp	Cys	Val	Pro	Glu	Gln	Val	Ile	Ala	Glu	Ala
	210					215					220				
Ile	Arg	Lys	Lys	Thr	Arg	Ser	Met	Leu	Leu	Ser	Ser	Glu	Gln	Leu	Lys
225					230					235					240
Leu	Cys	Val	Leu	Glu	Tyr	Gln	Gly	Lys	Tyr	Ile	Leu	Lys	Val	Cys	Gly
			245						250					255	
Cys	Asp	Glu	Tyr	Phe	Leu	Glu	Lys	Tyr	Pro	Leu	Ser	Gln	Tyr	Lys	Tyr
		260						265					270		
Ile	Arg	Ser	Cys	Ile	Met	Leu	Gly	Arg	Met	Pro	Asn	Leu	Met	Leu	Met
	275						280					285			
Ala	Lys	Glu	Ser	Leu	Tyr	Ser	Gln	Leu	Pro	Ile	Asp	Ser	Phe	Thr	Met
	290					295					300				
Pro	Ser	Tyr	Ser	Arg	Arg	Ile	Ser	Thr	Ala	Thr	Pro	Tyr	Met	Asn	Gly
305					310					315					320
Glu	Thr	Ser	Thr	Lys	Ser	Leu	Trp	Val	Ile	Asn	Ser	Ala	Leu	Arg	Ile
			325						330					335	
Lys	Ile	Leu	Cys	Ala	Thr	Tyr	Val	Asn	Val	Asn	Ile	Arg	Asp	Ile	Asp
		340						345					350		
Lys	Ile	Tyr	Val	Arg	Thr	Gly	Ile	Tyr	His	Gly	Gly	Glu	Pro	Leu	Cys
	355					360						365			
Asp	Asn	Val	Asn	Thr	Gln	Arg	Val	Pro	Cys	Ser	Asn	Pro	Arg	Trp	Asn
	370					375					380				
Glu	Trp	Leu	Asn	Tyr	Asp	Ile	Tyr	Ile	Pro	Asp	Leu	Pro	Arg	Leu	Ala
385					390					395					400
Arg	Leu	Cys	Leu	Ser	Ile	Cys	Ser	Val	Lys	Gly	Arg	Lys	Gly	Ala	Lys
			405						410					415	
Glu	Glu	His	Cys	Pro	Leu	Ala	Trp	Gly	Asn	Ile	Asn	Leu	Phe	Asp	Tyr
			420					425					430		
Thr	Asp	Thr	Leu	Val	Ser	Gly	Lys	Met	Ala	Leu	Asn	Leu	Trp	Pro	Val
	435					440						445			
Pro	His	Gly	Leu	Glu	Asp	Leu	Leu	Asn	Pro	Ile	Gly	Val	Thr	Gly	Ser
	450					455					460				
Asn	Pro	Asn	Lys	Glu	Thr	Pro	Cys	Leu	Glu	Leu	Glu	Phe	Asp	Trp	Phe
465					470					475					480
Ser	Ser	Val	Val	Lys	Phe	Pro	Asp	Met	Ser	Val	Ile	Glu	Glu	His	Ala
			485						490					495	
Asn	Trp	Ser	Val	Ser	Arg	Glu	Ala	Gly	Phe	Ser	Tyr	Ser	His	Thr	Gly
			500					505					510		
Leu	Ser	Asn	Arg	Leu	Ala	Arg	Asp	Asn	Glu	Leu	Arg	Glu	Asn	Asp	Lys

Glu	Gln	Leu	Arg	Ala	Leu	Cys	Thr	Arg	Asp	Pro	Leu	Ser	Glu	Ile	Thr
	530					535					540				
Glu	Gln	Glu	Lys	Asp	Phe	Leu	Trp	Ser	His	Arg	His	Tyr	Cys	Val	Thr
545					550					555					560
Ile	Pro	Glu	Ile	Leu	Pro	Lys	Leu	Leu	Leu	Ser	Val	Lys	Trp	Asn	Ser
				565					570						575
Arg	Asp	Glu	Val	Ala	Gln	Met	Tyr	Cys	Leu	Val	Lys	Asp	Trp	Pro	Pro
			580					585					590		
Ile	Lys	Pro	Glu	Gln	Ala	Met	Glu	Leu	Leu	Asp	Cys	Asn	Tyr	Pro	Asp
			595				600					605			
Pro	Met	Val	Arg	Ser	Phe	Ala	Val	Arg	Cys	Leu	Glu	Lys	Tyr	Leu	Thr
	610				615						620				
Asp	Asp	Lys	Leu	Ser	Gln	Tyr	Leu	Ile	Gln	Leu	Val	Gln	Val	Leu	Lys
625					630				635						640
Tyr	Glu	Gln	Tyr	Leu	Asp	Asn	Leu	Leu	Val	Arg	Phe	Leu	Leu	Lys	Lys
				645					650					655	
Ala	Leu	Thr	Asn	Gln	Arg	Ile	Gly	His	Phe	Phe	Phe	Trp	His	Leu	Lys
			660					665					670		
Ser	Glu	Met	His	Asn	Lys	Thr	Val	Ser	Gln	Arg	Phe	Gly	Leu	Leu	Leu
		675					680					685			
Glu	Ser	Tyr	Cys	Arg	Ala	Cys	Gly	Met	Tyr	Leu	Lys	His	Leu	Asn	Arg
	690					695					700				
Gln	Val	Glu	Ala	Met	Glu	Lys	Leu	Ile	Asn	Leu	Thr	Asp	Ile	Leu	Lys
705					710				715						720
Gln	Glu	Lys	Lys	Asp	Glu	Thr	Gln	Lys	Val	Gln	Met	Lys	Phe	Leu	Val
				725					730					735	
Glu	Gln	Met	Arg	Gln	Pro	Asp	Phe	Met	Asp	Ala	Leu	Gln	Gly	Phe	Leu
			740					745					750		
Ser	Pro	Leu	Asn	Pro	Ala	His	Gln	Leu	Gly	Asn	Leu	Arg	Leu	Glu	Glu
		755					760					765			
Cys	Arg	Ile	Met	Ser	Ser	Ala	Lys	Arg	Pro	Leu	Trp	Leu	Asn	Trp	Glu
	770					775					780				
Asn	Pro	Asp	Ile	Met	Ser	Glu	Leu	Leu	Phe	Gln	Asn	Asn	Glu	Ile	Ile
785					790				795						800
Phe	Lys	Asn	Gly	Asp	Asp	Leu	Arg	Gln	Asp	Met	Leu	Thr	Leu	Gln	Ile
				805					810					815	
Ile	Arg	Ile	Met	Glu	Asn	Ile	Trp	Gln	Asn	Gln	Gly	Leu	Asp	Leu	Arg
			820					825					830		
Met	Leu	Pro	Tyr	Gly	Cys	Leu	Ser	Ile	Gly	Asp	Cys	Val	Gly	Leu	Ile
		835					840					845			
Glu	Val	Val	Arg	Asn	Ser	His	Thr	Ile	Met	Gln	Ile	Gln	Cys	Lys	Gly
	850					855					860				
Gly	Leu	Lys	Gly	Ala	Leu	Gln	Phe	Asn	Ser	His	Thr	Leu	His	Gln	Trp
865			</												

Lys Gln Met Asn Asp Ala His His Gly Gly Trp Thr Thr Lys Met Asp
1045 1050 1055
Trp Ile Phe His Thr Ile Lys Gln His Ala Leu Asn
1060 1065

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1070 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Cys Phe Ser Phe Ile Met Pro Pro Ala Met Ala Asp Ile Leu Asp
1 5 10 15
Ile Trp Ala Val Asp Ser Gln Ile Ala Ser Asp Gly Ser Ile Pro Val
20 25 30
Asp Phe Leu Leu Pro Thr Gly Ile Tyr Ile Gln Leu Glu Val Pro Arg
35 40 45
Glu Ala Thr Ile Ser Tyr Ile Lys Gln Met Leu Trp Lys Gln Val His
50 55 60
Asn Tyr Pro Met Phe Asn Leu Leu Met Asp Ile Asp Ser Tyr Met Phe
65 70 75 80
Ala Cys Val Asn Gln Thr Ala Val Tyr Glu Glu Leu Glu Asp Glu Thr
85 90 95
Arg Arg Leu Cys Asp Val Arg Pro Phe Leu Pro Val Leu Lys Leu Val
100 105 110
Thr Arg Ser Cys Asp Pro Gly Glu Lys Leu Asp Ser Lys Ile Gly Val
115 120 125
Leu Ile Gly Lys Gly Leu His Glu Phe Asp Ser Leu Lys Asp Pro Glu
130 135 140
Val Asn Glu Phe Arg Arg Lys Met Arg Lys Phe Ser Glu Glu Lys Ile
145 150 155 160
Leu Ser Leu Val Gly Leu Ser Trp Met Asp Trp Leu Lys Gln Thr Tyr
165 170 175
Pro Pro Glu His Glu Pro Ser Ile Pro Glu Asn Leu Glu Asp Lys Leu
180 185 190
Tyr Gly Gly Lys Leu Ile Val Ala Val His Phe Glu Asn Cys Gln Asp
195 200 205
Val Phe Ser Phe Gln Val Ser Pro Asn Met Asn Pro Ile Lys Val Asn
210 215 220
Glu Leu Ala Ile Gln Lys Arg Leu Thr Ile His Gly Lys Glu Asp Glu
225 230 235 240
Val Ser Pro Tyr Asp Tyr Val Leu Gln Val Ser Gly Arg Val Glu Tyr
245 250 255
Val Phe Gly Asp His Pro Leu Ile Gln Phe Gln Tyr Ile Arg Asn Cys
260 265 270
Val Met Asn Arg Ala Leu Pro His Phe Ile Leu Val Glu Cys Cys Lys
275 280 285
Ile Lys Lys Met Tyr Glu Gln Glu Met Ile Ala Ile Glu Ala Ala Ile
290 295 300
Asn Arg Asn Ser Ser Asn Leu Pro Leu Pro Leu Pro Pro Lys Lys Thr
305 310 315 320
Arg Ile Ile Ser His Val Trp Glu Asn Asn Asn Pro Phe Gln Ile Val
325 330 335
Leu Val Lys Gly Asn Lys Leu Asn Thr Glu Glu Thr Val Lys Val His
340 345 350
Val Arg Ala Gly Leu Phe His Gly Thr Glu Leu Leu Cys Lys Thr Ile
355 360 365
Val Ser Ser Glu Val Ser Gly Lys Asn Asp His Ile Trp Asn Glu Pro
370 375 380

Leu	Glu	Phe	Asp	Ile	Asn	Ile	Cys	Asp	Leu	Pro	Arg	Met	Ala	Arg	Leu
385					390					395					400
Cys	Phe	Ala	Val	Tyr	Ala	Val	Leu	Asp	Lys	Val	Lys	Thr	Lys	Lys	Ser
				405					410					415	
Thr	Lys	Thr	Ile	Asn	Pro	Ser	Lys	Tyr	Gln	Thr	Ile	Arg	Lys	Ala	Gly
			420					425					430		
Lys	Val	His	Tyr	Pro	Val	Ala	Trp	Val	Asn	Thr	Met	Val	Phe	Asp	Phe
		435					440					445			
Lys	Gly	Gln	Leu	Arg	Thr	Gly	Asp	Ile	Ile	Leu	His	Ser	Trp	Ser	Ser
	450					455					460				
Phe	Pro	Asp	Glu	Leu	Glu	Glu	Met	Leu	Asn	Pro	Met	Gly	Thr	Val	Gln
465					470					475					480
Thr	Asn	Pro	Tyr	Thr	Glu	Asn	Ala	Thr	Ala	Leu	His	Val	Lys	Phe	Pro
				485					490					495	
Glu	Asn	Lys	Lys	Gln	Pro	Tyr	Tyr	Tyr	Pro	Pro	Phe	Asp	Lys	Ile	Ile
			500					505					510		
Glu	Lys	Ala	Ala	Glu	Ile	Ala	Ser	Ser	Asp	Ser	Ala	Asn	Val	Ser	Ser
		515					520					525			
Arg	Gly	Gly	Lys	Lys	Phe	Leu	Pro	Val	Leu	Lys	Glu	Ile	Leu	Asp	Arg
	530					535					540				
Asp	Pro	Leu	Ser	Gln	Leu	Cys	Glu	Asn	Glu	Met	Asp	Leu	Ile	Trp	Thr
545					550					555					560
Leu	Arg	Gln	Asp	Cys	Arg	Glu	Ile	Phe	Pro	Gln	Ser	Leu	Pro	Lys	Leu
				565					570					575	
Leu	Leu	Ser	Ile	Lys	Trp	Asn	Lys	Leu	Glu	Asp	Val	Ala	Gln	Leu	Gln
			580					585					590		
Ala	Leu	Leu	Gln	Ile	Trp	Pro	Lys	Leu	Pro	Pro	Arg	Glu	Ala	Leu	Glu
		595					600					605			
Leu	Leu	Asp	Phe	Asn	Tyr	Pro	Asp	Gln	Tyr	Val	Arg	Glu	Tyr	Ala	Val
	610					615					620				
Gly	Cys	Leu	Arg	Gln	Met	Ser	Asp	Glu	Glu	Leu	Ser	Gln	Tyr	Leu	Leu
625					630					635					640
Gln	Leu	Val	Gln	Val	Leu	Lys	Tyr	Glu	Pro	Phe	Leu	Asp	Cys	Ala	Leu
				645					650					655	
Ser	Arg	Phe	Leu	Leu	Glu	Arg	Ala	Leu	Gly	Asn	Arg	Arg	Ile	Gly	Gln
			660					665					670		
Phe	Leu	Phe	Trp	His	Leu	Arg	Ser	Glu	Val	His	Ile	Pro	Ala	Val	Ser
		675					680					685			
Val	Gln	Phe	Gly	Val	Ile	Leu	Glu	Ala	Tyr	Cys	Arg	Gly	Ser	Val	Gly
	690					695					700				
His	Met	Lys	Val	Leu	Ser	Lys	Gln	Val	Glu	Ala	Leu	Asn	Lys	Leu	Lys
705					710					715					720
Thr	Leu	Asn	Ser	Leu	Ile	Lys	Leu	Asn	Ala	Val	Lys	Leu	Asn	Arg	Ala
				725					730					735	
Lys	Gly	Lys	Glu	Ala	Met	His	Thr	Cys	Leu	Lys	Gln	Ser	Ala	Tyr	Arg
			740					745					750		
Glu	Ala	Leu	Ser	Asp	Leu	Gln	Ser	Pro	Leu	Asn	Pro	Cys	Val	Ile	Leu
		755					760					765			
Ser	Glu	Leu	Tyr	Val	Glu	Lys	Cys	Lys	Tyr	Met	Asp	Ser	Lys	Met	Lys
	770					775					780				
Pro	Leu	Trp	Leu	Val	Tyr	Asn	Asn	Lys	Val	Phe	Gly	Glu	Asp	Ser	Val
785					790					795					800
Gly	Val	Ile	Phe	Lys	Asn	Gly	Asp	Asp	Leu	Arg	Gln	Asp	Met	Leu	Thr
			805						810					815	
Leu	Gln	Met	Leu	Arg	Leu	Met	Asp	Leu	Leu	Trp	Lys	Glu	Ala	Gly	Leu
			820					825					830		
Asp	Leu	Arg	Met	Leu	Pro	Tyr	Gly	Cys	Leu	Ala	Thr	Gly	Asp	Arg	Ser
		835					840					845			
Gly	Leu	Ile	Glu	Val	Val	Ser	Thr	Ser	Glu	Thr	Ile	Ala	Asp	Ile	Gln
	850					855					860				
Leu	Asn	Ser	Ser	Asn	Val	Ala	Ala	Ala	Ala	Ala	Phe	Asn	Lys	Asp	Ala
865					870					875					880
Leu	Leu	Asn	Trp	Leu	Lys	Glu	Tyr	Asn	Ser	Gly	Asp	Asp	Leu	Asp	Arg
				885					890					895	
Ala	Ile	Glu	Glu	Phe	Thr	Leu	Ser	Cys	Ala	Gly	Tyr	Cys	Val	Ala	Ser

				245					250					255	
Leu	Met	Asp	Ile	Pro	Glu	Ser	Gln	Ser	Glu	Gln	Asp	Phe	Val	Leu	Arg
			260					265					270		
Val	Cys	Gly	Arg	Asp	Glu	Tyr	Leu	Val	Gly	Glu	Thr	Pro	Ile	Lys	Asn
		275					280					285			
Phe	Gln	Trp	Val	Arg	His	Cys	Leu	Lys	Asn	Gly	Glu	Glu	Ile	His	Val
	290					295					300				
Val	Leu	Asp	Thr	Pro	Pro	Asp	Pro	Ala	Leu	Asp	Glu	Val	Arg	Lys	Glu
305					310					315					320
Glu	Trp	Pro	Leu	Val	Asp	Asp	Cys	Thr	Gly	Val	Thr	Gly	Tyr	His	Glu
				325					330					335	
Gln	Leu	Thr	Ile	His	Gly	Lys	Asp	His	Glu	Ser	Val	Phe	Thr	Val	Ser
			340					345					350		
Leu	Trp	Asp	Cys	Asp	Arg	Lys	Phe	Arg	Val	Lys	Ile	Arg	Gly	Ile	Asp
		355					360					365			
Ile	Pro	Val	Leu	Pro	Arg	Asn	Thr	Asp	Leu	Thr	Val	Phe	Val	Glu	Ala
	370					375					380				
Asn	Ile	Gln	His	Gly	Gln	Gln	Val	Leu	Cys	Gln	Arg	Arg	Thr	Ser	Pro
385				390						395					400
Lys	Pro	Phe	Thr	Glu	Glu	Val	Leu	Trp	Asn	Val	Trp	Leu	Glu	Phe	Ser
				405					410					415	
Ile	Lys	Ile	Lys	Asp	Leu	Pro	Lys	Gly	Ala	Leu	Leu	Asn	Leu	Gln	Ile
			420					425					430		
Tyr	Cys	Gly	Lys	Ala	Pro	Ala	Leu	Ser	Ser	Lys	Ala	Ser	Ala	Glu	Ser
		435					440					445			
Pro	Ser	Ser	Glu	Ser	Lys	Gly	Lys	Val	Arg	Leu	Leu	Tyr	Tyr	Val	Asn
	450					455					460				
Leu	Leu	Leu	Ile	Asp	His	Arg	Phe	Leu	Leu	Arg	Arg	Gly	Glu	Tyr	Val
465				470						475					480
Leu	His	Met	Trp	Gln	Ile	Ser	Gly	Lys	Gly	Glu	Asp	Gln	Gly	Ser	Phe
				485					490					495	
Asn	Ala	Asp	Lys	Leu	Thr	Ser	Ala	Thr	Asn	Pro	Asp	Lys	Glu	Asn	Ser
			500					505					510		
Met	Ser	Ile	Ser	Ile	Leu	Leu	Asp	Asn	Tyr	Cys	His	Pro	Ile	Ala	Leu
		515					520					525			
Pro	Lys	His	Gln	Pro	Thr	Pro	Asp	Pro	Glu	Gly	Asp	Arg	Val	Arg	Ala
	530					535					540				
Glu	Met	Pro	Asn	Gln	Leu	Arg	Lys	Gln	Leu	Glu	Ala	Ile	Ile	Ala	Thr
545				550						555					560
Asp	Pro	Leu	Asn	Pro	Leu	Thr	Ala	Glu	Asp	Lys	Glu	Leu	Leu	Trp	His
				565					570					575	
Phe	Arg	Tyr	Glu	Ser	Leu	Lys	His	Pro	Lys	Ala	Tyr	Pro	Lys	Leu	Phe
			580					585					590		
Ser	Ser	Val	Lys	Trp	Gly	Gln	Gln	Glu	Ile	Val	Ala	Lys	Thr	Tyr	Gln
		595													

Lys	Leu	Glu	Asn	Leu	Gln	Asn	Ser	Gln	Leu	Pro	Glu	Ser	Phe	Arg	Val
770						775					780				
Pro	Tyr	Asp	Pro	Gly	Leu	Lys	Ala	Gly	Ala	Leu	Ala	Ile	Glu	Lys	Cys
785					790					795					800
Lys	Val	Met	Ala	Ser	Lys	Lys	Lys	Pro	Leu	Trp	Leu	Glu	Phe	Lys	Cys
			805						810					815	
Ala	Asp	Pro	Thr	Ala	Leu	Ser	Asn	Glu	Thr	Ile	Gly	Ile	Ile	Phe	Lys
			820					825					830		
His	Gly	Asp	Asp	Leu	Arg	Gln	Asp	Met	Leu	Ile	Leu	Gln	Ile	Leu	Arg
		835					840					845			
Ile	Met	Glu	Ser	Ile	Trp	Glu	Thr	Glu	Ser	Leu	Asp	Leu	Cys	Leu	Leu
	850					855					860				
Pro	Tyr	Gly	Cys	Ile	Ser	Thr	Gly	Asp	Lys	Ile	Gly	Met	Ile	Glu	Ile
865					870					875					880
Val	Lys	Asp	Ala	Thr	Thr	Ile	Ala	Lys	Ile	Gln	Gln	Ser	Thr	Val	Gly
			885						890					895	
Asn	Thr	Gly	Ala	Phe	Lys	Asp	Glu	Val	Leu	Asn	His	Trp	Leu	Lys	Glu
			900					905					910		
Lys	Ser	Pro	Thr	Glu	Glu	Lys	Phe	Gln	Ala	Ala	Val	Glu	Arg	Phe	Val
		915					920					925			
Tyr	Ser	Cys	Ala	Gly	Tyr	Cys	Val	Ala	Thr	Phe	Val	Leu	Gly	Ile	Gly
	930					935					940				
Asp	Arg	His	Asn	Asp	Asn	Ile	Met	Ile	Thr	Glu	Thr	Gly	Asn	Leu	Phe
945					950					955					960
His	Ile	Asp	Phe	Gly	His	Ile	Leu	Gly	Asn	Tyr	Lys	Ser	Phe	Leu	Gly
			965						970					975	
Ile	Asn	Lys	Glu	Arg	Val	Pro	Phe	Val	Leu	Thr	Pro	Asp	Phe	Leu	Phe
			980					985					990		
Val	Met	Gly	Thr	Ser	Gly	Lys	Lys	Thr	Ser	Pro	His	Phe	Gln	Lys	Phe
		995					1000					1005			
Gln	Asp	Ile	Cys	Val	Lys	Ala	Tyr	Leu	Ala	Leu	Arg	His	His	Thr	Asn
1010						1015					1020				
Leu	Leu	Ile	Ile	Leu	Phe	Ser	Met	Met	Leu	Met	Thr	Gly	Met	Pro	Gln
025					1030					1035					1040
Leu	Thr	Ser	Lys	Glu	Asp	Ile	Glu	Tyr	Ile	Arg	Asp	Ala	Leu	Thr	Val
			1045						1050					1055	
Gly	Lys	Asn	Glu	Glu	Asp	Ala	Lys	Lys	Tyr	Phe	Leu	Asp	Gln	Ile	Glu
			1060					1065					1070		
Val	Cys	Arg	Asp	Lys	Gly	Trp	Thr	Val	Gln	Phe	Asn	Trp	Phe	Leu	His
	1075					1080						1085			
Leu	Val	Leu	Gly	Ile	Lys	Gln	Gly	Glu	Lys	His	Ser	Ala			
1090						1095						1100			

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ile	Phe	Lys	Asn	Gly	Asp	Asp	Leu	Arg	Gln	Asp	Met	Leu
1				5								10

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

His Ile Asp Phe Gly His
1 5